RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/796,669*

Source: *I-FWD*

Date Processed by STIC: *3/18/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, **PLEASE USE THE CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1D03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/796,669

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics   Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFWO

RAW SEQUENCE LISTING   DATE: 03/18/2004
PATENT APPLICATION: US/10/796,669   TIME: 15:02:36

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\03172004\J796669.raw

```
     3 <110> APPLICANT: Jin-Town Wang
     4         Tzu-Lung Lin
W--> 5 <120> TITLE OF INVENTION: A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/796,669
C--> 6 <141> CURRENT FILING DATE: 2004-03-09
W--> 0 <130> FILE REFERENCE:          please insert
W--> 6 <160> NUMBER OF SEQ ID: 5
     7 <170> SOFTWARE: MICROSOFT WORD 2000
```

delete, please do not use alpha numeric headings in a sequence.

Does Not Comply
Corrected Diskette Needed
(pg. 1-7)

ERRORED SEQUENCES

```
E--> 8 <210> SEQ ID NO: SEQ ID NO:1
     9 <211> LENGTH: LENGTH 5               delete, same error
    10 <212> TYPE: DNA
    11 <213> ORGANISM: ORGANISM: Helicobacter pylori
E--> 13 <400> SEQUENCE: SEQUENCE:1     delete
E--> 14 ccatc        5   delete
E--> 16 <210> SEQ ID NO: SEQ ID NO:2
    17 <211> LENGTH: LENGTH 1617          delete, same error
    18 <212> TYPE: DNA
    19 <213> ORGANISM: ORGANISM: Helicobacter pylori
    21 <300> PUBLICATION INFORMATION:
    22 <308> DATABASE ACCESSION NO: DDBJ/EMBL/Genbank;Accession No.:AB118944
W--> 24 <300> PUBLICATION INFORMATION: SEQUENCE:2    insert here
E--> 25 atg act aaa aaa ccg gca cga aaa att tta agc ttt tca
    26  acc acc atg cga aac cct aaa   60
E--> 28 aga ata gga caa ttt tta gct gtt tta gga aag ttt gaa
    29  aat caa atc ctt aaa tct tca   120
E--> 31 ata atc atg caa att atc aaa tcc gtt ttg gct cat agg
    32  ctt tat aga cct act tct ctc   180
E--> 34 aat caa aat aaa gaa ttg aaa gaa aaa ttt gac tcc aat
    35  gaa tat gtc ttt agc gat gaa   240
E--> 37 gag tta gaa cgc att ata gaa ata tcc cca caa aat cat
    38  aaa gaa atg ggc ttt gag cat   300
E--> 40 gga tgg gaa agc cgg ttt gac act tgg tat aag ctt atg
    41  tgt gag ttt ggt ttt tgc tac   360
E--> 43 tat gca aaa tat gag aaa ata ctc atc agc gat agc gct
    44  aag atg ctt att ctt gct tat   420
E--> 46 tac aat aaa gaa aac gat gct ttt aaa gaa agc gtt gat
    47  gaa agc gta gtt ggg gct ata   480
E--> 49 ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct
    50  tac aaa aag aat tta aac cat   540
```

(please see attached sample sequence listing)

IF you include <308> with a response, then you must include <309> with a response.

— please group the nucleotides in sets of 10, for example

Please see item #1 on error summary sheet.

Please see item #4 on error summary sheet.

```
file:///C:\CRF4\Outhold\VsrJ796669.htm       ttntagtagt tgtaaggatt            3/18/04
```

```
        RAW SEQUENCE LISTING              DATE: 03/18/2004
        PATENT APPLICATION:  US/10/796,669    TIME: 15:02:36

            Input Set : A:\PTO.DA.txt
            Output Set: N:\CRF4\03172004\J796669.raw
```

```
E--> 52  aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa cga
     53  ctc aaa aat gcc cat cta acc   600
E--> 55  ccc cta tct gtc aaa gaa atc cct att tta ctt tgt tgg
     56  aaa gac gat aac gct aat ggg   660
E--> 58  ctt tat gac tac att att cgt tta aga caa gaa atc gtt
     59  act atc aat aaa aca gaa ttc   720
E--> 61  agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa
     62  ctt tta gaa agt gtt aat aaa   780
E--> 64  aca cga ttt aaa atg agc caa atc act aac gaa gcc gtt
     65  gat gaa tac att aga aaa atg   840
E--> 67  cgt att aca gga ctt att tca ttg cgt ggt aat ggt agg
     68  ttt att gat att aat act aat   900
E--> 70  gaa aat aat aaa ata gat tac att tta caa acc cat aag
     71  gct ttt aaa ggg gat tat tta   960
E--> 73  aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac
     74  atg gcg atc gtg gat agc ttt   1020
E--> 76  ctt gtt agt gtt act cca atc agc gct aat gag agc gtt
     77  aaa tca agc aaa ttg aat gaa   1080
E--> 79  cta gca aac act tat act aaa gat ttt atc aag caa gaa
     80  tta ctc att act tgt aac aag   1140
E--> 82  caa gaa tca aaa gat agt ttt tta aga ctc att gat aaa
     83  cct tta cgc tta gaa ttt tta   1200
E--> 85  agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc
     86  gtg ata ccc aat tat aaa agc   1260
E--> 88  gat gat gaa ggc ttg ccc gta tac aca gca agc ggt aat
     89  aaa cct gat att gta gct atg   1320
E--> 91  gac aca aaa gcc caa agt tat ata gaa gtg agc ttg att
     92  aga gac aga agt caa agt acc   1380
E--> 94  ttg gaa atg ata cct att gcc aga cat tta aaa gaa ttg
     95  att aaa aat agc acc gat att   1440
E--> 97  aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat
     98  gat gat gcc aaa gaa tat gcg   1500
E--> 100 gaa ttt gcc caa ttc aaa gac aat att aat ata tgt tgt
     101 tat gct att aat gat ttt atc   1560
E--> 103 aaa aaa gta gaa aac agc ata gaa tgg tta cag atc aat
E--> 104 gac cat ttg aaa gct taa   1617
E--> 107 <210> SEQ ID NO: SEQ ID NO:3
     108 <211> LENGTH: LENGTH:538
     109 <212> TYPE: PRT
     110 <213> ORGANISM: ORGANISM: Helicobacter pylori
E--> 113 <400> SEQUENCE: SEQUENCE:3
     114 Met Thr Lys Lys Pro Ala Arg Lys Ile Leu Ser Phe Ser
E--> 115 Thr Thr Met
E--> 116 1      5      10
E--> 117 15
     119 Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu
E--> 120 Gly Lys Phe
E--> 121 20     25     30
     123 Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile
```

(Handwritten annotations:)

- please group Nucleotide in sets of 10.
- ← See item #1 on error summary sheet.
- SEQ ID NO:3 — delete,
- LENGTH:538 — delete
- ↑Do not use alpha numeric headings.
- SEQUENCE:3 — delete
- ORGANISM: (circled)
- ← please see item #1 on error summary sheet,

RAW SEQUENCE LISTING   DATE: 03/18/2004
PATENT APPLICATION: US/10/796,669   TIME: 15:02:36

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\03172004\J796669.raw

```
E--> 124  Ile Lys Ser
E--> 125 35      40      45
     127 Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn
E--> 128  Gln Asn Lys
E--> 129 50      55      60
     131 Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe
E--> 132  Ser Asp Glu
E--> 133 65      70      75
E--> 134    80
     136 Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His
E--> 137  Lys Glu Met
E--> 138 85      90      95
     140 Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp
E--> 141  Tyr Lys Leu
E--> 142 100     105     110
     144 Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu
E--> 145  Lys Ile Leu
E--> 146 115     120     125
     148 Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr
E--> 149  Asn Lys Glu
E--> 150 130     135     140
     152 Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val
E--> 153  Gly Ala Ile
E--> 154 145     150     155
E--> 155    160
     157 Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro
E--> 158  Tyr Lys Lys
E--> 159 165     170     175
     161 Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser
E--> 162  Leu Leu Lys
E--> 163 180     185     190
     165 Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys
E--> 166  Glu Ile Pro
E--> 167 195     200     205
     169 Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu
E--> 170  Tyr Asp Tyr
E--> 171 210     215     220
     173 Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys
E--> 174  Thr Glu Phe
E--> 175 225     230     235
E--> 176    240
     178 Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys
E--> 179  Leu Leu Glu
E--> 180 245     250     255
     182 Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr
E--> 183  Asn Glu Ala
E--> 184 260     265     270
     186 Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu
E--> 187  Ile Ser Leu
```

— please see item #1 on error summary sheet.

RAW SEQUENCE LISTING   DATE: 03/18/2004
PATENT APPLICATION: US/10/796,669   TIME: 15:02:36

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03172004\J796669.raw**

```
E--> 188 275        280         285
     190 Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu
E--> 191  Asn Asn Lys
E--> 192 290         295         300
     194 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly
E--> 195  Asp Tyr Leu
E--> 196 305         310         315
E--> 197    320
     200 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr
E--> 201  Met Ala Ile
E--> 202 325         330         335
     204 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala
E--> 205  Asn Glu Ser
E--> 206 340         345         350
     208 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr
E--> 209  Thr Lys Asp
E--> 210 355         360         365
     212 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln
E--> 213  Glu Ser Lys
E--> 214 370         375         380
     216 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu
E--> 217  Glu Phe Leu
E--> 218 385         390         395
E--> 219    400
     221 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser
E--> 222  Val Ile Pro
E--> 223 405         410         415
     225 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr
E--> 226  Ala Ser Gly
E--> 227 420         425         430
     229 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln
E--> 230  Ser Tyr Ile
E--> 231 435         440         445
     233 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu
E--> 234  Glu Met Ile
E--> 235 450         455         460
     237 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser
E--> 238  Thr Asp Ile
E--> 239 465         470         475
E--> 240    480
     243 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His
E--> 244  Asp Asp Ala
E--> 245 485         490         495
     247 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile
E--> 248  Asn Ile Cys
E--> 249 500         505         510
     251 Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn
E--> 252  Ser Ile Glu
E--> 253 515         520         525
```

(handwritten note, right margin:) same errors, see item #1 on error summary sheet

```
                    RAW SEQUENCE LISTING          DATE: 03/18/2004
                    PATENT APPLICATION:  US/10/796,669     TIME: 15:02:36

                    Input Set : A:\PTO.DA.txt
                    Output Set: N:\CRF4\03172004\J796669.raw
```

same error (handwritten)

```
        255 Trp Leu Gln Ile Asn Asp His Leu Lys Ala
E--> 256 530      535
        259 <210> SEQ ID NO: 4
        260 <211> LENGTH 780
        261 <212> TYPE: DNA
        262 <213> ORGANISM: ORGANISM: Helicobacter pylori
        264 <300> PUBLICATION INFORMATION:
        265 <308> DATABASE ACCESSION NO.: DDBJ/EMBL/Genbank;Accession No.:AB118944
W--> 267 <300> PUBLICATION INFORMATION: 4
E--> 268 atg ggg caa gac gct gat ttt aaa gcg ctt gaa gaa ctg
        269  aaa gaa tac ttt aat caa gct  60
E--> 271 tta aag cta gaa gaa aat tat ttt agc caa cat ttt agc
        272  aac aag ttt ttc agc tat aaa  120
E--> 274 gat tgt gtc aaa atc ggt agc att aga gag cat ata gaa
        275  agc tta aac tta gat aaa tta  180
E--> 277 aat aaa gat att tta tta aca agc ctg att tat tca atg
        278  gat aag ata gct aac acg gta  240
E--> 280 ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa
        281  gat aga ttt att ttt gag ctt  300
E--> 283 att agc cct ata aaa cat gat aaa aat atc atg ata gag
        284  aga aaa aac gct aac gaa ttg  360
E--> 286 gct aaa acc tta aaa ata gac tta gtc ttt att gat cct
        287  cca tac aat tca agg caa tac  420
E--> 289 agc cgg ttt tat cat ctc tat gaa aac cta gtg cag tgg
        290  aaa aaa ccc aaa ctc tat gga  480
E--> 292 aca gct tta aag cca tca tgc gag aac atg agc gaa tat
        293  tgc cgc tct aat gcc aag aaa  540
E--> 295 gaa ttg agc gat tta att gaa aaa cta gat tgt aaa agg
        296  att gct tta act tat aat aat  600
E--> 298 acc tat aac tct aag tct agc tct tcg caa aat aaa ata
        299  ggc ttt aaa gat tta gtg gaa  660
E--> 301 att ttg agt caa aaa gga aaa tta agc gtt aaa gaa aag
        302  gct cat agt ttt ttt aat tca  720
E--> 304 gga aaa act gat ttt aaa gag cat aaa gaa ttt tta ttt
        305  ata gtg gaa gtg aaa cct tga  780
E--> 308 <210> SEQ ID NO: SEQ ID NO:5
        309 <211> LENGTH: LENGTH 846
        310 <212> TYPE: DNA
        311 <213> ORGANISM: ORGANISM Helicobacter pylori
        313 <300> PUBLICATION INFORMATION:
        314 <308> DATABASE ACCESSION NO.: DDBJ/EMBL/Genbank;Accession No.:AB118944
W--> 316 <300> PUBLICATION INFORMATION: SEQUENCE:5
E--> 317 atg cca caa ctc aat aag cta ttc cca aat aac att aat
        318  caa ttt att gag cct ttt gtg  60
E--> 320 ggt ggg ggt agc gtg ttt tta aac act aag gct aag aga
        321  tac tta gct aat gac ata gat  120
E--> 323 act aat att atc aat tta cat aaa act tta agc aag ttc
        324  aat gtt tgt gag ctt ttt gat  180
E--> 326 gaa ttg tct aaa att atc att cat tat ggc ttg tct ttc
```

Handwritten annotations:
- *delete, same error* (near line 260)
- *IF you include <308> then you must include <309> with response.* (right margin)
- *same errors* (middle right)
- *delete, same errors* (near line 309)
- *same errors, please insert also <309>* (right margin near 314)
- *same errors* (near line 323)

RAW SEQUENCE LISTING   DATE: 03/18/2004
PATENT APPLICATION: US/10/796,669   TIME: 15:02:36

           Input Set : A:\PTO.DA.txt
           Output Set: N:\CRF4\03172004\J796669.raw

         327   tct ttt aag ggg att atg gcc   240
E-->   329 cct gat gaa tta aaa aaa caa tat ata aaa act tac tac
         330   gcc aaa tac aat aaa ata gct   300
E-->   332 tat gaa aaa cta agg gct gat ttt aac tcc aat caa aac
         333   aac atg ctt tat ttg tat ttg   360
E-->   335 ctt tta att tat gga ttt aat cac atg att aga ttt aat
         336   tct aaa ggg ctt ttt aat tta   420
E-->   338 cct gtg ggt aat gtg gat ttc aat gaa aat gtt tat aat
         339   gcc cta aaa aac tac ata gat   480
E-->   341 ttt ata cag caa aac acc att att ttt cac aat gat gat
         342   tat att gat ttt ctt aac cac   540
E-->   344 acc act tat tta aaa gat gat tat gtt tat ttt gac ccc
         345   cct tat tta atc tcc aat agt   600
E-->   347 gaa tac aac aag tta tgg gat agc gat aat gag ata gcc
         348   tta tat ggt gtt tta gat agc   660
E-->   350 cta gat aaa aag gga gtt tta ttt ggt ata act aat ctt
         351   att tat cac aag gga gag act   720
E-->   353 aat ttt att tta aaa gaa tgg gct aaa aaa tat tat att
         354   ttt aat atc aaa agt aat tat   780
E-->   356 atc agt tat aat gac aat act att aaa gaa gat agt gaa
         357   gaa atc ttt gta act aat tat   840
         359 agg tga   846
E-->   362 1

same errs

delete

VERIFICATION SUMMARY   DATE: 03/18/2004
PATENT APPLICATION: **US/10/796,669**   TIME: 15:02:37

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03172004\J796669.raw**

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:8 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:8 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:14 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:5 SEQ:0
L:16 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:24 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:0
L:24 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:25 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:0
M:254 Repeated in SeqNo=0
L:104 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:1617 SEQ:0
L:107 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:113 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:115 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=0
L:256 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:538 SEQ:0
L:267 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:4
L:268 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:4
M:254 Repeated in SeqNo=4
L:308 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:316 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:0
L:316 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:4
L:317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:0
M:254 Repeated in SeqNo=0
L:362 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:846 SEQ:0

10/796,669 ①

(Sample Sequence Listing)

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<110>        Smith, John;   Smithgene Inc.

<120>        Example of a Sequence Listing

<130>        01-00001

<140>        PCT/EP98/00001
<141>        1998-12-31

<150>        US 08/999,999
<151>        1997-10-15

<160>        4

<170>        PatentIn version 2.0

<210>        1
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<212>        DNA
<213>        Paramecium sp.

<220>
<221>        CDS
<222>        (279)...(389)

<300>
<301>        Doe, Richard
<302>        Isolation and Characterization of a Gene Encoding a
             Protease from Paramecium sp.
<303>        Journal of Genes
<304>        1
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<306>        1-7
<307>        1988-06-31
<308>        123456
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<400>        1
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agggagagtg    tcttgaccct   cctctgcctt   tgcagcttca   caggcaggca   ggcaggcagc       120

tgatgtggca    attgctggca   gtgccacagg   cttttcagcc   aggcttaggg   tgggttccgc       180

cgcggcgcgg    cggcccctct   cgcgctcctc   tcgcgcctct   ctctcgctct   cctctcgctc       240
```

(Sample Sequence Listing)

```
ggacctgatt   aggtgagcag   gaggaggggg   cagttagc        atg   gtt   tca   atg   ttc   agc   296
                                                        Met   Val   Ser   Met   Phe   Ser
                                                         1                      5


ttg   tct   ttc   aaa   tgg   cct   gga   ttt   tgt   ttg   ttt   gtt   tgt   ttg   ttc   caa   344
Leu   Ser   Phe   Lys   Trp   Pro   Gly   Phe   Cys   Leu   Phe   Val   Cys   Leu   Phe   Gln
                  10                      15                            20


tgt   ccc   aaa   gtc   ctc   ccc   tgt   cac   tca   tca   ctg   cag   ccg   aat   ctt       389
Cys   Pro   Lys   Val   Leu   Pro   Cys   His   Ser   Ser   Leu   Gln   Pro   Asn   Leu
            25                      30                            35
```

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<210>        2
<211>        37
<212>        PRT
<213>        Paramecium sp.


<400>        2
Met   Val   Ser   Met   Phe   Ser   Leu   Ser   Phe   Lys   Trp   Pro   Gly   Phe   Cys   Leu
 1                      5                      10                            15


Phe   Val   Cys   Leu   Phe   Gln   Cys   Pro   Lys   Val   Leu   Pro   Cys   His   Ser   Ser
                  20                      25                            30


Leu   Gln   Pro   Asn   Leu
                  35
```

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<210>        3
<211>        11
<212>        PRT
<213>        Artificial Sequence


<220>
<223>        Designed peptide based on size and polarity to act as a
             linker between the alpha and beta chains of Protein XYZ.

<400>        3
Met   Val   Asn   Leu   Glu   Pro   Met   His   Thr   Glu   Ile
 1                      5                            10


<210>        4
<400>        4
000
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[Annex VIII follows]